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OM nucleic - nucleic search, using sw model

Run on: January 22, 2004, 12:55:27 ; Search time 50 Seconds

(without alignments)

2886.646 Million cell updates/sec

Title: US-09-541-462b-1

Perfect score: 327

Sequence: 1 atggcgagcagcgatggatgt.....tccaaaagtggcactag 327

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*

2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253.6	77.6	3208	4	US-09-780-016-27
2	90	27.5	301	4	US-09-313-294A-492
3	31	9.5	2408	1	US-08-608-241-1
4	31	9.5	2408	2	US-08-922-182-1
5	31	9.5	2408	2	US-08-919-953-1
6	31	9.5	2408	3	US-09-192-983-1
7	30	9.2	648	4	US-09-599-360B-27
8	29.2	8.9	2951	1	US-08-386-727-7
9	29.2	8.9	2951	2	US-08-600-452A-7
10	28.6	8.7	648	4	US-09-252-991A-4236
11	28.6	8.7	723	4	US-09-252-991A-9470
12	28.6	8.7	1080	1	US-07-598-873-1
13	28.6	8.7	1080	1	US-08-073-425-1
14	28.6	8.7	1080	1	US-08-396-531-1
15	28.6	8.7	1488	4	US-09-252-991A-4168
16	28.6	8.7	2618	4	US-09-857-556A-25
17	28.4	8.7	3420	1	US-08-117-491-25
18	28.4	8.7	3420	1	US-08-271-364A-6
19	28.4	8.7	3420	2	US-08-222-715B-25
20	28.4	8.7	4707	1	US-08-004-139B-2
21	28.4	8.7	4707	2	US-08-811-492-2
22	28.4	8.7	4707	5	PCT-US96-10545A-2
23	28.4	8.7	35524	3	US-08-923-137-1
24	28.2	8.6	31880	4	US-09-453-702B-242
25	28	8.6	42931	4	US-08-311-731A-129
26	27.6	8.4	903	4	US-09-107-532A-2965
27	27.6	8.4	70000	4	US-09-851-896-3

ALIGNMENTS

RESULT 1

US-09-780-016-27

; Sequence 27, Application US/09780016

; Patent No. 6509456

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Abuin, Alejandro

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6509456el Human Proteases and

; FILE REFERENCE: Polynucleotides Encoding the Same

; CURRENT APPLICATION NUMBER: US/09/780,016

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,294

; PRIOR FILING DATE: 2000-02-11

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 3208

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-780-016-27

Query Match 77.6%; Score 253.6; DB 4; Length 3208;

Best Local Similarity 98.5%; Pred. No. 4.2e-78;

Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 68 AAGTGAAGAATGGGAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGATACTGTG 127

DB 2765 AAAAAAAAAAATGGAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGATACTGTG 2824

QY 128 CCATCTGCAGGAACACACATTATGGATCTTTGATAGAAATGTCAAGCTAACAGGCGTCCG 187

DB 2825 CCATCTGCAGGAACACACATTATGGATCTTTGATAGAAATGTCAAGCTAACAGGCGTCCG 2884

QY 188 CTACTTCAGACAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACT 247

DB 2885 CTACTTCAGACAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACT 2944

QY 248 GCATCTCTCGTGGCTCAAAACACAGAGGTGTGTCATTGGACAAACAGAGTGGGAAT 307

DB 2945 GCATCTCTCGTGGCTCAAAACACAGAGGTGTGTCATTGGACAAACAGAGTGGGAAT 3004

QY 308 TCCAAAGTATGGCACTAG 327

DB 3005 TCCAAAGTATGGCACTAG 3024

Sequence 141, App  
Sequence 141, App  
Sequence 176, App  
Sequence 176, App  
Sequence 3, Appli  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 5445, Ap  
Sequence 5507, Ap  
Sequence 5507, Ap  
Sequence 5468, Ap  
Sequence 5435, Ap  
Sequence 21, Appli  
Sequence 1, Appli  
Sequence 19, Appli  
Sequence 22, Appli  
Sequence 5309, Ap  
Sequence 15934, A







```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07662/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-600-452A-7

Query Match      8.9%; Score 29.2; DB 2; Length 2951;
Best Local Similarity 62.2%; Pred. No. 5.3;
Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 3 GCGCGCAGCGATGGATGTGATACCCGAGCGCACCAACAGCGCGCGGCGGAAGAGCG 62
Db 151 GCGCGCAGCGCGCGGCGAGGTAGAACAGAGCCCCCGACAGCAATGCCAGCAGGGAATG 92
QY 63 CTTTGAAGTGAATA 76
Db 91 TTTTGGACTGAC 78

RESULT 10
US-09-252-991A-4236/c
; Sequence 4236, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4236
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4236

Query Match      8.7%; Score 28.6; DB 4; Length 648;
Best Local Similarity 54.2%; Pred. No. 4;
Matches 58; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 16 GATGTGATACCCGAGCGCGCACCAACAGCGCGCGGCGGAAGAGCGCTTTGAAGTGA 75
Db 509 GAGTGCAGAGTGTGACCGCAAGTTTCATGCGTGAGATCGAAGAGCACTGGAAGCAAA 450
QY 76 AAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATAA 122
Db 449 GAAGCGGACCTCATGCTGCTGAGCGCGGCTGACGTATGGAATA 403

RESULT 11
US-09-252-991A-9470/c
; Sequence 9470, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9470
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9470

Query Match      8.7%; Score 28.6; DB 4; Length 723;
Best Local Similarity 48.5%; Pred. No. 4.3;
Matches 79; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 10 GCGATGGATGTGGATACCCGAGCGCGCACCAACAGCGCGCGGCGGAAGAGCGCTTTGAA 69
Db 651 GAGTTGCCAGTCGACCGCGGCATCGTCACTCCCTGGCGAAGCGCGCAACTGCTCGCG 592
QY 70 GTGAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATTAACCTGTGCC 129
Db 591 CGGCACCGAGCGATCGGAGCGCGCTCGAGGACCACTACCGCGCCCTTGATGTTCTCTGC 532
QY 130 ATCTGCAGGAACCACTATTATGATCTTTGCATAGATGTCAAG 172
Db 531 ATGCGCGGCTCCGGCGTATCCAGGGTCCCATGGAAGGACAG 489

RESULT 12
US-07-598-873-1/c
; Sequence 1, Application US/07598873
; Patent No. 5254800
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: GRIERSON, DONALD
; APPLICANT: RAY, JOHN A
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/598,873
; FILING DATE: 19901019
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum
; STRAIN: Ailsa Craig
; DEVELOPMENTAL STAGE: Ripening
; US-07-598-873-1
Query Match      8.7%; Score 28.6; DB 1; Length 1080;
Best Local Similarity 61.3%; Pred. No. 5.2;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 221 TCTGTAACCATGCTTTTCCACTGCATCTCTCGTGGCTCAAAACACGACGGTGT 280
Db 742 TCTTTAACTTTCTTGATCAATTCAACTGCATATGTCCTGGATTGGAACATAACAAACCT 683

QY 281 GTCCATTGGACAACA 295
Db 682 GCTTTTGATACAACA 668

RESULT 14
US-08-396-531-1/c
; Sequence 1, Application US/08396531
; Patent No. 5744364
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: GRIERSON, DONALD
; APPLICANT: RAY, JOHN A
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Ninth Floor, 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,531
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,037
; FILING DATE: 16-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum
; STRAIN: Ailsa Craig
; DEVELOPMENTAL STAGE: Ripening
; US-08-396-531-1
Query Match      8.7%; Score 28.6; DB 1; Length 1080;
Best Local Similarity 61.3%; Pred. No. 5.2;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 221 TCTGTAACCATGCTTTTCCACTGCATCTCTCGTGGCTCAAAACACGACGGTGT 280
Db 742 TCTTTAACTTTCTTGATCAATTCAACTGCATATGTCCTGGATTGGAACATAACAAACCT 683

QY 281 GTCCATTGGACAACA 295
Db 682 GCTTTTGATACAACA 668

RESULT 13
US-08-073-425-1/c
; Sequence 1, Application US/08073425
; Patent No. 5569829
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: BONIWELL, JEREMY M.
; APPLICANT: GRIERSON, DONALD
; APPLICANT: RAY, JOHN A
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,425
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DEEVER, DONALD B.
; REGISTRATION NUMBER: 23,048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum
; STRAIN: Ailsa Craig
; DEVELOPMENTAL STAGE: Ripening
; US-08-073-425-1
Query Match      8.7%; Score 28.6; DB 1; Length 1080;
Best Local Similarity 61.3%; Pred. No. 5.2;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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RESULT 15
US-09-252-991A-4168/c
; Sequence 4168, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4168
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4168

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Query Match      8.7%; Score 28.6; DB 4; Length 1488;
Best Local Similarity 54.2%; Pred. No. 6.1;
Matches 58; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 16 GATGTGATACCCGAGCGGACCAACAGCGCGGCGGCAAGAGCGCTTTGAAGTGAAA 75
Db 846 GACGTGCAGAGCTGACCCAGAGTTTCATCGGTGAGATCGAAGGCACTGGAGCCAAA 787

QY 76 AAGTGGATGCCAGTAGCCCTCTGGGCGCTGGGATATTGTGTTGATAA 122
Db 786 GAAGCGGACCTCATGCTCTCTGAGCGCGGCTGACGTCATGGAATA 740

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Search completed: January 22, 2004, 13:55:30  
Job time : 52 secs

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Result	No.	Query			DB	ID	Description
		Score	Match	Length			
C	1	325	99.4	476	11	US-09-918-995-17191	Sequence 17191, App
	2	321.8	98.4	4543	15	US-10-198-846-11311	Sequence 11311, App
	3	302.4	92.5	380	10	US-09-960-352-4677	Sequence 4677, App
	4	301.2	92.1	5347	13	US-10-240-965-99	Sequence 99, App
	5	296.8	90.8	5111	15	US-10-205-823-382	Sequence 382, App
	6	253.6	77.6	3208	9	US-09-780-016-27	Sequence 27, App
C	7	253.6	77.6	3208	15	US-10-214-811-27	Sequence 27, App
	8	205.8	62.9	439	11	US-09-918-995-14771	Sequence 14771, App
	9	183.8	56.2	175561	15	US-10-017-721-3	Sequence 3, App
	10	173	52.9	390	9	US-09-770-791-20	Sequence 20, App
	11	157.4	48.1	418	9	US-09-962-436-220	Sequence 220, App
	12	138.8	42.4	415	15	US-10-198-846-2493	Sequence 2493, App
C	13	102.2	31.3	812	12	US-10-264-049-751	Sequence 751, App
	14	76.4	23.4	271	9	US-09-294-093B-735	Sequence 735, App
	15	76	23.2	336	10	US-09-764-864-39	Sequence 39, App

Db 194 CTGTGCCATCTGCAGCAACACATTATGGATCTTTGCATAGATGTCAGAGTAAACCAAGCG 253  
Qy 183 GTCCGCTACTTCAAGAGAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTCACTT 242  
Db 254 GTCCGCTACTTCAAGAGAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTCACTT 313  
Qy 243 CCACTGCATCTCTCGTGGCTCAAAACACAGCAGAGTGTGTCCATTGGCAACACAGAGAGTG 302  
Db 314 CCACTGCATCTCTCGTGGCTCAAAACACAGCAGAGTGTGTCCATTGGCAACACAGAGAGTG 373  
Qy 303 GGAATTCCTCAAAAGTATGGGCACTAG 327  
Db 374 GGAATTCCTCAAAAGTATGGGCACTAG 398

RESULT 2  
US-10-198-846-11311/c  
; Sequence 11311, Application US/10198846  
; Publication No. US20030099974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; PRIOR FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11311  
; LENGTH: 4543  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-198-846-11311

Query Match 98.4%; Score 321.8; DB 15; Length 4543;  
Best Local Similarity 99.4%; Pred. No. 7.4e-104;  
Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGCGCAGCATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCG 62  
Db 1089 GCGCGCAGCATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCG 1030  
Qy 63 CTTTGAAGTGAAGTGAATGCAGTACGCCCTCTGGGCTGGGATATTGTGTTGATAA 122  
Db 1029 CTTTGAAGTGAAGTGAATGCAGTACGCCCTCTGGGCTGGGATATTGTGTTGATAA 970  
Qy 123 CTGTGCCATCTGCAGGAACACATTATGGATCTTTGCATAGATGTCAAGCTAACCAAGC 182  
Db 969 CTGTGCCATCTGCAGGAACACATTATGGATCTTTGCATAGATGTCAAGCTAACCAAGC 910  
Qy 183 GTCCGCTACTTCAAGAGAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTCACTT 242  
Db 909 GTCCGCTACTTCAAGAGAGTGTACTGTCCATGGGAGTCTGTAAACCATGCTTTTCACTT 850  
Qy 243 CCACTGCATCTCTCGTGGCTCAAAACACAGCAGAGTGTGTCCATTGGCAACACAGAGTG 302  
Db 849 CCACTGCATCTCTCGTGGCTCAAAACACAGCAGAGTGTGTCCATTGGCAACACAGAGTG 790  
Qy 303 GGAATTCCTCAAAAGTATGGGCACTAG 327  
Db 789 GGAATTCCTCAAAAGTATGGGCACTAG 765

RESULT 3  
US-09-960-352-4677  
; Sequence 4677, Application US/09960352

; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 4677  
; LENGTH: 380  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 20-LIB34-034-Q1-E1-E7  
US-09-960-352-4677

Query Match 92.5%; Score 302.4; DB 10; Length 380;  
Best Local Similarity 96.6%; Pred. No. 2e-97;  
Matches 309; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 8 CAGCGATGATGTGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTG 67  
Db 2 CAGCGATGATGTGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTG 61  
Qy 68 AAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATACTGTG 127  
Db 62 AAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATACTGTG 121  
Qy 128 CCATCTGCAGGAACACACATTATGGATCTTTGCATAGATGTCAAGCTAACCAAGCGCTCG 187  
Db 122 CCATCTGCAGGAACACACATTATGGATCTTTGCATAGATGTCAAGCTAACCAAGCGCTCG 181  
Qy 188 CTACTTCAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCACT 247  
Db 182 CTACTTCAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTCACT 241  
Qy 248 GCATCTCTCGTGGCTCAAAACACAGCAGAGTGTGTCCATTGGCAACACAGAGTGGGAAT 307  
Db 242 GCATCTCTCGTGGCTCAAAACACAGCAGAGTGTGTCCATTGGCAACACAGAGTGGGAAT 301  
Qy 308 TCCAAAAGTATGGGCACTAG 327  
Db 302 TCCAAAAGTATGGGCACTAG 321

RESULT 4  
US-10-240-965-99/c  
; Sequence 99, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAI, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 99  
; LENGTH: 5347  
; TYPE: DNA  
; ORGANISM: Homo sapiens

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FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 364940.19
US-10-240-965-99

Query Match      92.1%; Score 301.2; DB 13; Length 5347;
Best Local Similarity 98.7%; Pred. No. 1.8e-96;
Matches 314; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGC-GGGCAAGAAGC 61
DB 519 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGGCGGCGCAAGAAGC 460

QY 62 GCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATA 121
DB 459 GCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATA 400

QY 122 ACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 181
DB 399 ACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 340

QY 182 CGTCCGCTACTTCCAGAGAGTGTACTGTCCATGGGAGTCTCTAACCATGCTTTTCACT 241
DB 339 CGTCCGCTACTTCCAGAGAGTGTACTGTCCATGGGAGTCTCTAACCATGCTTTTCACT 280

QY 242 TCCACTGCATCTCTCGCTGCTGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAGT 301
DB 279 TCCACTGCATCTCTCGCTGCTGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAGT 220

QY 302 GCGAATTCGAAAGTAGT 319
DB 219 GCGAATTCGAAAGTAGT 202

RESULT 5
US-10-205-823-382/c
; Sequence 382, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wensey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 5111
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-382

Query Match      92.1%; Score 301.2; DB 13; Length 5347;
Best Local Similarity 98.7%; Pred. No. 1.8e-96;
Matches 314; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGC-GGGCAAGAAGC 61
DB 519 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGGCGGCGCAAGAAGC 460

QY 62 GCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATA 121
DB 459 GCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATA 400

QY 122 ACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 181
DB 399 ACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 340

QY 182 CGTCCGCTACTTCCAGAGAGTGTACTGTCCATGGGAGTCTCTAACCATGCTTTTCACT 241
DB 339 CGTCCGCTACTTCCAGAGAGTGTACTGTCCATGGGAGTCTCTAACCATGCTTTTCACT 280

QY 242 TCCACTGCATCTCTCGCTGCTGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAGT 301
DB 279 TCCACTGCATCTCTCGCTGCTGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAGT 220

QY 302 GCGAATTCGAAAGTAGT 319
DB 219 GCGAATTCGAAAGTAGT 202

RESULT 6
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. US20020004591A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020004591A1 Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27

Query Match      77.6%; Score 253.6; DB 9; Length 3208;
Best Local Similarity 98.5%; Pred. No. 1.5e-79;
Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 68 AAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGTG 127
DB 2765 AAAAAAAAAAATGGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGTG 2824

QY 128 CCATCTGCAGGAACCAACATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGGCGTCCG 187
DB 2825 CCATCTGCAGGAACCAACATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGGCGTCCG 2884

QY 188 CTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 247
DB 2885 CTACTTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 2944

QY 248 GCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAGTGGAAAT 307
DB 2945 GCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAGTGGAAAT 3004

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QY 308 TCCAAAAGTATGGGCACTAG 327
Db 3005 TCCAAAAGTATGGGCACTAG 3024

RESULT 7
US-10-214-811-27
; Sequence 27, Application US/10214811
; Publication No. US20030023062A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030023062A1el Human Proteases and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/214,811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-214-811-27

Query Match 77.6%; Score 253.6; DB 15; Length 3208;
Best Local Similarity 98.5%; Pred. No. 1.5e-79;
Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 68 AAGTGAAGAAGTGAATGAGTATGGATCTTGGCCCTGGGATATGGTTGATACTGTG 127
Db 2765 AAAAAAATGAATGAGTATGGATCTTGGCCCTGGGATATGGTTGATACTGTG 2824

QY 128 CCATCTGCAGGAACCACTATGGATCTTGGATAGAAATGTCAAGTAAACCAAGGCGTCCG 187
Db 2825 CCATCTGCAGGAACCACTATGGATCTTGGATAGAAATGTCAAGTAAACCAAGGCGTCCG 2884

QY 188 CTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 247
Db 2885 CTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 2944

QY 248 GCATCTCTCGCTCGCTCAAAACACGACAGTGTGTCTTGGACACAGAGAGTGGGAAT 307
Db 2945 GCATCTCTCGCTCGCTCAAAACACGACAGTGTGTCTTGGACACAGAGAGTGGGAAT 3004

QY 308 TCCAAAAGTATGGGCACTAG 327
Db 3005 TCCAAAAGTATGGGCACTAG 3024

RESULT 8
US-09-918-995-14771
; Sequence 14771, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054

QY 308 TCCAAAAGTATGGGCACTAG 327
Db 3005 TCCAAAAGTATGGGCACTAG 3024

Query Match 62.9%; Score 205.8; DB 11; Length 439;
Best Local Similarity 99.0%; Pred. No. 7.3e-63;
Matches 207; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 GTGGAATGAGTATGGGCTCTGGGCTGGGATATTTGGTTGATACTGTGCCATCTGCAG 137
Db 231 GTGGAATGAGTATGGGCTCTGGGCTGGGATATTTGGTTGATACTGTGCCATCTGCAG 290

QY 138 GAACACATTTATGGATCTTTGCATAGATGTCAAGCTAACCAAGGCTCGCTACTTTCAG 197
Db 291 GAACACATTTATGGATCTTTGCATAGATGTCAAGCTAACCAAGGCTCGCTACTTTCAG 350

QY 198 AGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACTGCTCTCG 257
Db 351 AGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACTGCTCTCG 410

QY 258 CTGGCTCAAAACACGACAGGTGTGTCCAT 286
Db 411 CTGGCTCAAAACACGACAGGTGTGTCCAT 439

RESULT 9
US-10-017-721-3
; Sequence 3, Application US/10017721
; Publication No. US20030096248A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; APPLICANT: Daley, George
; APPLICANT: Bolk, Stacey
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-003
; CURRENT APPLICATION NUMBER: US/10/017,721
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,033
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/330,248
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 17561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-721-3

Query Match 56.2%; Score 183.8; DB 15; Length 17561;
Best Local Similarity 81.3%; Pred. No. 8.7e-54;
Matches 269; Conservative 0; Mismatches 42; Indels 20; Gaps 4;

QY 1 ATGGCGGCGAGCATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAG 60
Db 59458 ATGGCAGTGGCAATGGATGTGGATACCCCAAGAGTACCAACAGC-----AG 59504

QY 61 CGCTTTGAAGTGAAGTGAATGCAG-----TAGCCCTCTGGGCTGGGATATTGTGT 116
Db 59505 TCGTTTGAAGTGAAGTGAATGCAGTAGTACCCCTCTGGGCTGGGATATTGTGT 59564

QY 117 TGATAACTGTGCCATCTGCAGGAACCACTATATGATCTTTGCATAGATGTCAAGCTAA 176
Db 59565 TAATAACTGTGCCATCTGCAGGAATCACAGCATGGATC--TGCATTGAATGTCAAGCTAA 59622

QY 177 CCAGGCGTCCGCTACTTTCAGAAAGAGTGTACTCTCCATGGGAGTCTGTAAACCATGCTTT 236
Db 59623 CCAGAGTCTGCCATCTTTCAGAAAGTGTGTACCGTGTCAACCGGAGGCTGTAAACCGTCTTT 59682

QY 237 TCACCTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAG 296
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Query Match 42.4%; Score 138.8; DB 15; Length 415;

RESULT 11



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 13:34:15 ; Search time 55 Seconds  
(without alignments)  
866.716 Million cell updates/sec

Title: US-09-541-462B-2  
Perfect score: 616  
Sequence: 1 MAAMMDVTPSGTNSGAGKK.....KTRQVCPLDNREWEFKYGH 108

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-MODEL=frame.p2n.model -DEV=xlh  
-Q/cgn2\_1/USFTC\_spool/US09541462/runat\_22012004\_125829\_1552/app\_query.fasta\_1.263  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09541462 @CIGN 1.1.56 @runat\_22012004\_125829\_1552 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*  
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4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501.5	81.4	3208	4	US-09-780-016-27
2	262.5	42.6	301	4	Sequence 27, Appl
3	217	35.2	648	4	Sequence 492, App
C	4	90	14.6	8438	Sequence 27, Appl
	5	85	13.8	2339	Sequence 11, Appl
	6	85	13.8	2507	Sequence 11, Appl
	7	85	13.8	2517	Sequence 11, Appl
8	81	13.5	315	4	Sequence 7, Appl
9	81.5	13.2	4259	2	Sequence 7, Appl
10	81.5	13.2	4259	3	Sequence 2, Appl
11	80.5	13.1	804	3	Sequence 881, Appl
12	80	13.0	944	2	Sequence 4, Appl

13	80	13.0	1112	2	US-08-933-750C-97	Sequence 97, Appl
14	80	13.0	1112	3	US-09-234-613-97	Sequence 97, Appl
15	79.5	12.9	1683	1	US-07-945-283-3	Sequence 3, Appl
16	79	12.8	1470	4	US-09-663-600A-153	Sequence 153, App
17	79	12.8	1544	2	US-08-867-057-2	Sequence 2, Appl
18	79	12.8	1544	2	US-08-128-389-2	Sequence 2, Appl
19	79	12.8	1570	4	US-09-663-600A-59	Sequence 59, Appl
20	78	12.7	278	4	US-09-313-294A-756	Sequence 756, App
21	78	12.7	2146	4	US-09-620-312D-443	Sequence 443, App
22	77.5	12.6	617	4	US-09-280-116-115	Sequence 115, App
C	77.5	12.6	1830121	4	US-09-557-884-1	Sequence 1, Appl
C	77.5	12.6	1830121	4	US-09-643-990A-1	Sequence 1, Appl
23	76	12.3	621	4	US-09-364-206-28	Sequence 28, Appl
24	76	12.3	3911	4	US-09-423-890-1	Sequence 1, Appl
25	76	12.3	4693	3	US-09-359-756-1	Sequence 1, Appl
26	76	12.3	5253	4	US-09-423-890-7	Sequence 7, Appl
27	76	12.3	5253	4	US-08-628-829-3	Sequence 3, Appl
28	76	12.3	5539	4	US-09-599-360B-64	Sequence 64, Appl
29	75.5	12.3	1355	4	US-09-328-352-1185	Sequence 1185, App
30	75.5	12.3	1355	4	US-09-599-360B-64	Sequence 64, Appl
31	74.5	12.1	900	4	US-09-690-454-39	Sequence 39, Appl
32	74.5	12.1	1114	4	US-09-205-258-156	Sequence 156, App
33	74.5	12.1	1251	4	US-08-786-606-6	Sequence 6, Appl
34	74.5	12.1	1253	2	US-09-016-434-5	Sequence 5, Appl
35	74.5	12.1	1253	4	US-09-016-434-5	Sequence 5, Appl
C	74.5	12.1	1831	6	5215881-1	Patent No. 5215881
C	74.5	12.1	1831	6	5215881-3	Patent No. 5215881
36	74.5	12.1	2481	4	US-09-894-998A-35	Sequence 35, Appl
37	74.5	12.1	2481	4	US-09-313-294A-1763	Sequence 1763, App
38	74	12.0	266	4	US-09-801-876B-3	Sequence 3, Appl
39	74	12.0	148567	4	US-08-946-026-17	Sequence 17, Appl
40	74	12.0	148567	4	US-08-946-026-17	Sequence 17, Appl
41	73	11.9	1397	3	US-08-693-103B-7	Sequence 7, Appl
42	73	11.9	1656	3	US-08-693-103B-7	Sequence 7, Appl
43	73	11.9	1656	4	US-09-229-059-7	Sequence 7, Appl
44	73	11.9	1656	4	US-09-628-133-7	Sequence 7, Appl
45	72.5	11.8	666	1	US-08-018-977C-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-780-016-27  
; Sequence 27, Application US/09780016  
; Patent No. 6509456  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Abutin, Alejandro  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6509456el Human Proteases and  
; FILE REFERENCE: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0132-USA  
; CURRENT APPLICATION NUMBER: US/09/780,016  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,294  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 3208  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-780-016-27

Alignment Scores:  
Pred. No.: 5.03e-53  
Score: 501.50  
Percent Similarity: 95.70%  
Best Local Similarity: 94.62%  
Query Match: 81.41%  
Indels: 3  
Gaps: 1

US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)





APPLICANT: Cheung, Andrew K.  
 APPLICANT: Wesley, Ronald D.  
 TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants  
 TITLE OF INVENTION: Involving The EP0 and LIT Genes  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Curtis P. Ribando  
 STREET: 1815 No. 5352596th University Street  
 CITY: Peoria  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 61604

COMPUTER READABLE FORM: disk  
 MEDIUM TYPE: Floppy  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/945,283  
 FILING DATE: 19920911  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Ribando, Curtis P.  
 REGISTRATION NUMBER: 27976  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 309-685-4011 ext.513  
 TELEFAX: 309-685-4128

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 8438 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Pseudorabies virus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 622..6495  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1099, "g")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1267, "t")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1381, "c")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1566, "c")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(7010, "g")

US-07-945-283-1

Alignment Scores:  
 Pred. No.: 0.795  
 Score: 90.00  
 Percent Similarity: 40.86%  
 Best Local Similarity: 31.18%  
 Query Match: 14.61%  
 DB: 1

Length: 8438  
 Matches: 29  
 Conservative: 9  
 Mismatches: 25  
 Indels: 31  
 Gaps: 6

US-09-541-462B-2 (1-108) x US-07-945-283-1 (1-8438)

QY 6 AspValAsnThrProSerGlyValAcGlyLysLysArgPheGluValLys 25  
 Db 1568 GAGTGTAGATGGTCC-----GAGGTCCTGGTGG-TCCCGGGGGAGTTAGA 1522  
 QY 26 LysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCys 45

Db 1521 CGATCG-----TGGTCCGTCATG-----GACTGCCCATCTGC 1489  
 QY 46 ArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSer 65  
 Db 1488 -----CTGACGTC-----GCGGCCACC 1471  
 QY 66 GluGluCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHisCysIleSer 85  
 Db 1470 GAGGCGCAGACGCTGCG-----TGCATGCAACAAGTCTGTCTGGACTGCATCCAG 1420  
 QY 86 ArgTrpLeuLysThrArgGlnValCysProLeuAspAsn 98  
 Db 1419 CGCTGGACCTGACGACGACCGCTGCCCGCTGTGCAAT 1381

RESULT 5

US-09-268-140-11  
 ; Sequence 11, Application US/09268140  
 ; Patent No. 6268176  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gemmill, Robert M.  
 ; APPLICANT: Drabkin, Harry A.  
 ; TITLE OF INVENTION: TRC8 A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED  
 ; FILE REFERENCE: 93445-00004  
 ; CURRENT APPLICATION NUMBER: US/09/268,140  
 ; CURRENT FILING DATE: 2000-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/077,723  
 ; PRIOR FILING DATE: 1998-03-12  
 ; NUMBER OF SEQ ID NOS: 46  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 2339  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-268-140-11

Alignment Scores:  
 Pred. No.: 0.585  
 Score: 85.00  
 Percent Similarity: 40.48%  
 Best Local Similarity: 28.57%  
 Query Match: 13.80%  
 DB: 3

Length: 2339  
 Matches: 24  
 Conservative: 10  
 Mismatches: 22  
 Indels: 28  
 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

QY 20 LysArgPheGluValLysLysTrpAlaValAlaLeuTrpAlaTrpAspIle----- 37  
 Db 1635 CGTAGGACTGCTGCAAGAAATTAATTCACCTCCT-----GAAATAAAGGG 1682  
 QY 38 -----ValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeu 52  
 Db 1683 AGCCGCTTACAGAAATAAATGATGTATGTGCAATCTGCTATCATGAGTTT----- 1733  
 QY 53 CysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaLeuTrp 72  
 Db 1734 -----ACAACATCTGCTCGTATTACA----- 1754

QY 73 GlyValCysAsnHisAlaPheHisCysIleSerArgTrpLeuLysThrArgGln 92  
 Db 1755 ---CCGTGTAATCATTTATTTCCATGCACCTTGCCTTCGGAATGGCTGTACATTCAAGAT 1811  
 QY 93 ValCysProLeu 96  
 Db 1812 ACTTGTCCAATG 1823

RESULT 6

US-09-268-140-1  
 ; Sequence 1, Application US/09268140  
 ; Patent No. 6268176  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gemmill, Robert M.  
 ; APPLICANT: Drabkin, Harry A.

```
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)..(2232)
US-09-268-140-1
Alignment Scores:
Pred. No.: 0.642 Length: 2505
Score: 85.00 Matches: 24
Percent Similarity: 40.48% Conservative: 10
Best Local Similarity: 28.57% Mismatches: 22
Query Match: 13.80% Indels: 28
DB: 3 Gaps: 4
US-09-541-462B-2 (1-108) x US-09-268-140-1 (1-2505)
QY 20 LysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeu 37
Db 1801 CGTAGCACTGCTGTGAAGAAATAATTAATTCACCTCTCT-----GAAATAAAGGG 1848
QY 38 -----ValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeu 52
Db 1849 AGCCGCTTACAGAAATAATGATGATGTGCAATCTGTCATCATGAGTTT----- 1899
QY 53 CysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrp 72
Db 1900 -----ACAACATCTGCTCGTATTACA----- 1920
QY 73 GlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGln 92
Db 1921 ---CCGTGTAATCATATTATTTCCATGCACCTTTCGCTTCGGAATGGCTGTACATTCAAGAT 1977
QY 93 ValCysProLeu 96
Db 1978 ACTTGTCCAATG 1989
RESULT 7
US-09-268-140-7
; Sequence 7, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat unit
; LOCATION: (165)..(176)
US-09-268-140-7
Alignment Scores:
Pred. No.: 0.646 Length: 2517
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Score: 85.00 Matches: 24
Percent Similarity: 40.48% Conservative: 10
Best Local Similarity: 28.57% Mismatches: 22
Query Match: 13.80% Indels: 28
DB: 3 Gaps: 4
US-09-541-462B-2 (1-108) x US-09-268-140-7 (1-2517)
QY 20 LysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeu 37
Db 1813 CGTAGCACTGCTGTGAAGAAATAATTAATTCACCTCTCT-----GAAATAAAGGG 1860
QY 38 -----ValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeu 52
Db 1861 AGCCGCTTACAGAAATAATGATGATGTGCAATCTGTCATCATGAGTTT----- 1911
QY 53 CysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrp 72
Db 1912 -----ACAACATCTGCTCGTATTACA----- 1932
QY 73 GlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGln 92
Db 1933 ---CCGTGTAATCATATTATTTCCATGCACCTTTCGCTTCGGAATGGCTGTACATTCAAGAT 1989
QY 93 ValCysProLeu 96
Db 1990 ACTTGTCCAATG 2001
RESULT 8
US-09-325-932A-4
; Sequence 4, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-4
Alignment Scores:
Pred. No.: 0.0674 Length: 315
Score: 83.00 Matches: 17
Percent Similarity: 38.18% Conservative: 4
Best Local Similarity: 30.91% Mismatches: 20
Query Match: 13.47% Indels: 14
DB: 4 Gaps: 1
US-09-541-462B-2 (1-108) x US-09-325-932A-4 (1-315)
QY 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61
Db 74 TCGCGCGTGTGCTTCTCAAGTTTCGAAGACATT----- 106
QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe 81
Db 107 -----GAGATTCTCGGTTACTCCCAAGTGCAGGCATCCATTCACATC 151
QY 82 HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeu 96
Db 152 GATTGCATCGATTATTGCTTGAGAGACACTCAAGCTGCCCGCTC 196
RESULT 9
US-08-816-155B-2
; Sequence 2, Application US/08816155B
```

Patent No. 5990091  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,155B  
FILING DATE: 12-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2990  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4259 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-816-155B-2

Alignment Scores:  
Pred. No.: 3.64 Length: 4259  
Score: 81.50 Matches: 22  
Percent Similarity: 36.14% Conservative: 8  
Best Local Similarity: 26.51% Mismatches: 22  
Query Match: 13.23% Indels: 31  
DB: 2 Gaps: 4

US-09-541-462B-2 (1-108) x US-08-816-155B-2 (1-4259)

QY 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61  
Db 145 TGTAGCGTATGCTAGAAAGATATACGAAAGAAATAATAAACAA-----192  
QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyVal-----CysAsnHisAla 78  
Db 193 -----TATTCGGTATTTTACCAAAATGTAACACCGTG 225  
QY 79 PheHisPheHisCysIleSerArgTrpLeuLys-----ThrArgGln 92  
Db 226 TTTTGTCTGTATACACGTTGGATGCTCTATAATAAAGGTACGGATACCGAAGGT 285  
QY 93 ValCysPro-----LeuAspAsnArgGluTrpGluPhe 103  
Db 286 ACATGCTCTGTAGAACACAGTTTCTGTTTATATAGTGCTTAATAGGTACTGGATAGAC 345  
QY 104 GlnLysTyr 106  
Db 346 GATAAATAT 354

RESULT 10  
US-09-079-587-2  
Sequence 2, Application US/09079587  
Patent No. 6130066  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/816,155  
FILING DATE: 12-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2990  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4259 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-079-587-2

Alignment Scores:  
Pred. No.: 3.64 Length: 4259  
Score: 81.50 Matches: 22  
Percent Similarity: 36.14% Conservative: 8  
Best Local Similarity: 26.51% Mismatches: 22  
Query Match: 13.23% Indels: 31  
DB: 3 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-079-587-2 (1-4259)

QY 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla 61  
Db 145 TGTAGCGTATGCTAGAAAGATATACGAAAGAAATAATAAACAA-----192  
QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyVal-----CysAsnHisAla 78  
Db 193 -----TATTCGGTATTTTACCAAAATGTAACACCGTG 225  
QY 79 PheHisPheHisCysIleSerArgTrpLeuLys-----ThrArgGln 92  
Db 226 TTTTGTCTGTATACACGTTGGATGCTCTATAATAAAGGTACGGATACCGAAGGT 285  
QY 93 ValCysPro-----LeuAspAsnArgGluTrpGluPhe 103







GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 13:55:35 ; Search time 277 Seconds  
(without alignments)  
1394.436 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAANDVDTPSGTSGAGKK.....KTRQVCLDNREWEFKYGH 108

Scoring table:

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2356869 seqs, 1788235258 residues

Total number of hits satisfying chosen parameters: 4713738

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US09541462/runat\_22012004\_125830\_1585/app\_query.fasta\_1.263  
-DB=Published Applications NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09541462 @CGN\_1\_1\_221 @runat\_22012004\_125830\_1585  
-NCPUS=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NSG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTU5\_PUBCOMB.seq\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

US-09-918-995-17191  
; Sequence 17191, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows version 3.0  
; SEQ ID NO 17191  
; LENGTH: 476  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(476)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-17191

Sequence 17191, A  
Sequence 13111, A  
Sequence 4677, Ap  
Sequence 99, Appl  
Sequence 382, App  
Sequence 20, Appl  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 14771, A  
Sequence 3, Appl1  
Sequence 220, App  
Sequence 39, Appl  
Sequence 498, App  
Sequence 7, Appl1  
Sequence 7, Appl1  
Sequence 2493, Ap  
Sequence 847, Ap  
Sequence 847, Ap  
Sequence 847, Ap  
Sequence 847, Ap  
Sequence 27, Appl  
Sequence 27, Appl  
Sequence 735, App  
Sequence 2188, Ap  
Sequence 14, Appl  
Sequence 487, App  
Sequence 20531, A  
Sequence 38, Appl  
Sequence 22, App  
Sequence 497, App  
Sequence 19417, A  
Sequence 22557, A  
Sequence 20558, A  
Sequence 751, App  
Sequence 898, App  
Sequence 507, Appl  
Sequence 507, App  
Sequence 1952, Ap  
Sequence 13085, A  
Sequence 8855, Ap  
Sequence 459, App  
Sequence 21338, A





QY 104 GlnLysTyrGlyHis 108  
|||:|||||  
Db 304 CAAAGTATGGGCAC 318

## RESULT 4

US-10-240-965-99/c  
; Sequence 99, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAI, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 99  
; LENGTH: 5347  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030165924A1 364940.19  
US-10-240-965-99

## Alignment Scores:

Pred. No.: 1,276-67 Length: 5347  
Score: 573.00 Matches: 103  
Percent Similarity: 99.04% Conservative: 0  
Best Local Similarity: 99.04% Mismatches: 0  
Query Match: 93.02% Indels: 1  
DB: 13 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-240-965-99 (1-5347)

QY 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyVala-GlyLysLysArgPh 22  
|||:|||||  
Db 515 GCAGCGATGGATGTGGATACCCCGAGCGGCCAACAGCGCGCGCGGCAAGAGCGCTT 456  
|||:|||||  
QY 22 eGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCy 42  
|||:|||||  
Db 455 TGAAGTGAAAAAGTGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATAACTG 396  
|||:|||||  
QY 42 salalleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSe 62  
|||:|||||  
Db 395 TGCCATCTCGAGAACACCATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGCGTC 336  
|||:|||||  
QY 62 rAlaThrSerGluGluCysThrValalatrpglyValCysAsnHisAlaPheHis 82  
|||:|||||  
Db 335 CGTACTTCAGAAAGTGTACTCTCGCATGGGGAGTCTGTAACCATGCTTTTCACCTTCCA 276  
|||:|||||  
QY 82 sCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpG1 102  
|||:|||||  
Db 275 CTGCATCTCTCGTGGCTCAAAACACGACAGAGGTGTGTCTCCATTGGACACAGAGTGGGA 216  
|||:|||||  
QY 102 uPheGlnLys 105  
|||:|||||  
Db 215 ATTCCAAAAG 206  
|||:|||||

## RESULT 5

US-10-205-823-382/c  
; Sequence 382, Application US/10205823  
; Publication No. US20030108963A1  
; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gorbacheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Wansley, Angela M.  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Dustin  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 382  
; LENGTH: 5111  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-823-382

## Alignment Scores:

Pred. No.: 4,856-65 Length: 5111  
Score: 554.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 89.94% Indels: 0  
DB: 15 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-205-823-382 (1-5111)

QY 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLysArgPhe 22  
|||:|||||  
Db 296 GCAGCGATGGATGTGGATACCCCGAGCGGCCAACAGCGCGCGGCAAGAGCGCTT 237  
|||:|||||  
QY 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCy 42  
|||:|||||  
Db 236 GAAGTGAAAAAGTGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATAACTGT 177  
|||:|||||  
QY 43 AlaAlaCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62  
|||:|||||  
Db 176 GCCATCTCGAGAACACCATTTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGCGTCC 117  
|||:|||||  
QY 63 AlaThrSerGluGluCysThrValalatrpglyValCysAsnHisAlaPheHis 82  
|||:|||||  
Db 116 GTACTTTCAGAAAGTGTACTCTCGCATGGGGAGTCTGTAACCATGCTTTTCACCTTCCAC 57  
|||:|||||  
QY 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
|||:|||||  
Db 56 TGCATCTCTCGTGGCTCAAAACACGACAGAGGTGTGTCTCCATTGGACACAGAGAG 3  
|||:|||||

## RESULT 6

US-09-770-791-20  
; Sequence 20, Application US/09770791  
; Patent No. US20020062014A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jörn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.

```
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-20

Alignment Scores:
Pred. No.: 2 53e-61 Length: 390
Score: 515.50 Matches: 92
Percent Similarity: 83.19% Conservative: 7
Best Local Similarity: 77.31% Mismatches: 9
Query Match: 83.69% Indels: 11
DB: 9 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-770-791-20 (1-390)

QY 1 MetAlaAlaMetAspValaspThr-----ProSerGly----- 12
Db 20 TTAATGGCGACTAGACTCCGACGTTACCATGATTCTCGCGGAGAACGCTCCAGCAGC 79
QY 13 -----ThAsnSerGlyAlaGlyLysArgPheGluValLysLysTrpAsnAla 29
Db 80 GTAGCGCGCTGCTCTTCCAAACAAGAAAGCTAAGCGATTGCAATTAAGAAAGTGGAGCGCC 139
QY 30 ValAlaLeuTrpAlaTrpAspPheValValAspAsnCysAlaIleCysArgAsnHisIle 49
Db 140 GTTGCTCTCTGGGCTGGGATATCGTTGTGACAACTGTGCCATCTGCAGAAACACATC 199
QY 50 MetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThr 69
Db 200 ATGGATCTTTGTATCGAGTGTGAGGCTAATCAGGCCAGTCCACAAAGTGAAGTGCAC 259
QY 70 ValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLys 89
Db 260 GTAGCTTGGGGGTTTGGCAATCAGCGCTTCCACTTTTCACTGTCATCAGCAGATGGCTAAAG 319
QY 90 ThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGlyHis 108
Db 320 ACTCGTCAAGTTTGTCCATTGGGATTAACAGTGTGGGAGTTTTCAGAAATATGGTCA 376

RESULT 7
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. US20020004591A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
```

```
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020004591A1 Human Proteases and
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27

Alignment Scores:
Pred. No.: 4 09e-58 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.70% Conservative: 1
Best Local Similarity: 94.62% Mismatches: 1
Query Match: 81.41% Indels: 3
DB: 9 Gaps: 1

US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)

QY 16 GlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrp 35
Db 2752 GGAGCATATAAAAAAAAA-----AAAAAATGGAATGCAGTAGCCCTCTGGGCGCTGG 2802
QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
Db 2803 GATATTGTGTGTGTAACCTGTCATCTGCAGGAACCAACATTATGGATCTTTCATAGAA 2862
QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
Db 2863 TGTCAAGCTAACACGCGCTCCGCTACTTCAGAAAGAGTGTACTGTGCATGGGAGTCTGT 2922
QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95
Db 2923 AACCATGCTTTTCACTTCCACTGTCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTC 2982
QY 96 LeuAspAsnArgGluTrpGluPheGlnLysTrpGlyHis 108
Db 2983 TTGGACAACAGAGAGTGGGAATTCAAAAGATATGGGCAC 3021

RESULT 8
US-10-214-811-27
; Sequence 27, Application US/10214811
; Publication No. US20030023062A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214,811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
```

```

; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-214-811-27

Alignment Scores:
Pred. No.: 4,09e-58 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.70% Conservative: 1
Best Local Similarity: 94.62% Mismatches: 1
Query Match: 81.41% Indels: 3
DB: 15 Gaps: 1

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)

QY 16 GlyAlaGlyLysArgPheGluValLysTyrAsnAlaValAlaLeuTrpAlaTrp 35
DB 2752 GGAGCATAAATAAAAAA-----AAAATAAGTAAGCAGTACCCCTCTGGGCTGG 2802

QY 36 AspIleValAlaAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
DB 2803 GATATTGGTGTGATAACTGTGCCATCTGCAGGAACACATTATGATCTTTGCATAGAA 2862

QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
DB 2863 TGTCAAGCTAAACAGGCGTCCGCTACTTCAGAAAGAGTGTACTGTCGATGGGAGTCTGT 2922

QY 76 AsnHisAlaPheHisPheHisCysIleSerAtgTyrLeuLysThrArgGlnValCysPro 95
DB 2923 AACCATGCTTTTCACTTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGGTGTCCA 2982

QY 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
DB 2983 TTGGACAACAGAGAGTGGGAATTCGAAAGATATGGGCAC 3021

RESULT 9
US-09-918-995-14771
; Sequence 14771, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14771
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-14771

Alignment Scores:
Pred. No.: 7,74e-45 Length: 439
Score: 396.00 Matches: 67
Percent Similarity: 98.55% Conservative: 1
Best Local Similarity: 97.10% Mismatches: 1
Query Match: 64.29% Indels: 0
DB: 11 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-918-995-14771 (1-439)

QY 27 TrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArg 46
DB 232 TGGATGTCAGTATCCCTCTGGGCTGGGATATTGTGGATGATAACTGTGCCATCTGCAGS 291

QY 47 AsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGlu 66
DB 292 AACCATATTGATCTTTTGCATAGAAATGTCAAGCTAAACAGGCGTCCGCTACTTTCAGAA 351

QY 67 GluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArg 86
DB 352 GAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCATGTCATCTCTGC 411

QY 87 TrpLeuLysThrArgGlnValCysPro 95
DB 412 TGGCTCAAAACACGACGAGGTGTGTCCA 438

RESULT 10
US-10-017-721-3
; Sequence 3, Application US/10017721
; Publication No. US20030096248A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-003
; CURRENT APPLICATION NUMBER: US/10/017,721
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,033
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/330,248
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 175561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-721-3

Alignment Scores:
Pred. No.: 3,29e-35 Length: 175561
Score: 352.50 Matches: 75
Percent Similarity: 78.70% Conservative: 10
Best Local Similarity: 69.44% Mismatches: 20
Query Match: 57.22% Indels: 5
DB: 15 Gaps: 1

US-09-541-462B-2 (1-108) x US-10-017-721-3 (1-175561)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 59458 ATGGCAGTGGCAATGGATGTGGATACCCCAAGAAGTACCAACAGCAGTCTTTGAAGTAA 59517

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAsp 40
DB 59518 AAAAGTGAATGCAG-----TAGTAGCCCTCTGGGCTTGGGATGTTGTGTTAAT 59568

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValGluCysGlnAlaAsnGln 60
DB 59569 AACTGTGCCATCTGCAGGAATCACAGATGGATC--TGCATTGAATGTCAAGCTAACCAA 59626

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 59627 GAGTCTGCCATCTCAGAACTGTGTACCGTTGCACGGGAGCGCTGTAAACCGTCTTTTTC 59686

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 59687 TT-CACTGTCTCTCACTGGCTCAAAACACAAACAGCTGTGCGCTGTTGGACAACAGACAA 59745

QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 59746 TAGGAATTCCTCCAAAGTATGGACAC 59769

RESULT 11
US-09-962-436-220/C
; Sequence 220, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
```

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; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 220
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-220

Alignment Scores:
Pred. No.: 139e-30 Length: 418
Score: 292.00 Matches: 58
Percent Similarity: 84.42% Conservative: 7
Best Local Similarity: 75.32% Mismatches: 12
Query Match: 47.40% Indels: 2
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-962-436-220 (1-418)
QY 32 LeuTrpAlaTrpAspIleValValAspAsnCySAlaIleCySArgAsnHisIleMetAsp 51
Db 418 GTCTGGCGCTGGGATGTTGGTTAATACTGTGCCATCTGCAGGAATCACGATGGAT 359
QY 52 LeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla 71
Db 358 C--TGCATTCAATGTCAGCTAACCAAGAGCTCTGCCACITTCAGAAGTGTGTCACGTTGCA 301
QY 72 TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArg 91
Db 300 CGGGGAGCCCTGTAAACCGTGTCTTTTCATT-CACTGTCTCTCTCACTGGCTCAAAACACAA 242
QY 92 GlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
Db 241 CAGCTGTGCTGTGTGGCAACACAGACAAATAGGAATTCCTCAAGATGGACAC 191

RESULT 12
US-09-764-864-39
; Sequence 39 Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-39

Alignment Scores:
Pred. No.: 3.68e-30 Length: 836
Score: 292.00 Matches: 49
Percent Similarity: 64.95% Conservative: 14
Best Local Similarity: 50.52% Mismatches: 30
Query Match: 47.40% Indels: 4
DB: 10 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-764-864-39 (1-836)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30

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```
US-09-826-312-7
; Sequence 7, Application US/09826312
; Patent No. US20020042083A1
; GENERAL INFORMATION:
; APPLICANT: Iseakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613-1/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/826,312
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-312-7

Alignment Scores:
Pred. No.:          5,096-30      Length:          342
Score:              287.00      Matches:         48
Percent Similarity: 63.92%      Conservative:    14
Best Local Similarity: 49.48%    Mismatches:     31
Query Match:        46.59%      Indels:         4
DB:                  9          Gaps:           2

US-09-541-462B-2 (1-108) x US-09-826-312-7 (1-342)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30
Db 58 TCAGGCTCAACGTCGGGA---GGCGACAAGATGTTCTCCCTCAAGAAGTGGAAACCGGTG 114
QY 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 115 GCCATGTGAGCTGGGACGTGGAGTACGTACGTGCGCCATCTGCAGGTCAGGTGATG 174
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 175 GATGCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTTGTG 225
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 226 GTCTGGGGAGATGTAATCATTCCTTCCACAACACTGCTGCATGCTCCCTGGGTGAAACAG 285
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 286 AACAAATCGTCCCTCTCTGCCAGCAGGACTGGGTGGTCCCAAGAATCGGC 336

RESULT 15
US-10-108-767-7
; Sequence 7, Application US/10108767
; Publication No. US2003010474A1
; GENERAL INFORMATION:
; APPLICANT: Iseakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
; FILE REFERENCE: A-68613-5/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/108,767
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-767-7

Alignment Scores:
Pred. No.:          5,096-30      Length:          342
Score:              287.00      Matches:         48
Percent Similarity: 63.92%      Conservative:    14
Best Local Similarity: 49.48%    Mismatches:     31
Query Match:        46.59%      Indels:         4
DB:                  15         Gaps:           2

US-09-541-462B-2 (1-108) x US-10-108-767-7 (1-342)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30
Db 58 TCAGGCTCAACGTCGGGA---GGCGACAAGATGTTCTCCCTCAAGAAGTGGAAACCGGTG 114
QY 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 115 GCCATGTGAGCTGGGACGTGGAGTACGTACGTGCGCCATCTGCAGGTCAGGTGATG 174
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 175 GATGCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTTGTG 225
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
Db 226 GTCTGGGGAGATGTAATCATTCCTTCCACAACACTGCTGCATGCTCCCTGGGTGAAACAG 285
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 286 AACAAATCGTCCCTCTCTGCCAGCAGGACTGGGTGGTCCCAAGAATCGGC 336

Search completed: January 22, 2004, 15:27:26
Job time : 294 secs
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